

PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI Duesurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniela J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
XX WPI; 2002-010914/01.

XX Genomic sequence for *Listeria monocytogenes*, useful e.g. for treatment
PT and prevention of *Listeria* and related bacterial infections, and related
PT polypeptides.

XX Claim 6; SEQ ID NO 2071; 192pp; French.

XX The present invention relates to the genome sequence of *Listeria*
CC *monocytogenes* EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in *L.*
CC *monocytogenes* and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of *L. monocytogenes* and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate *L. monocytogenes*-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by *L.*
CC *monocytogenes* and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 277 AA;

Query Match 82.6%; Score 1203; DB 5; Length 277;
Best Local Similarity 82.4%; Pred. No. 6.5e-112;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;
QY 1 MAIKKYPITNGRRNMTSLDPAETTKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
Db 1 MAIKKYPITNGRRNMTSSDPAETTTTPKSLRPLPKKAGRNNOGKLTVRHHGGGHR 60
QY 61 QYRVDFKRNKOGINAKVDSIQYDPNRSANIALVYADGKRIYHCIAPKGLEVGQIVES 120
Db 61 QYRVDFKRNKOGIPGRVATIEYDPNRSANIALINYADGKR--YIIAAGLEVGQTYS 118
QY 121 GAEDATKVGNALPLONIPVGTIVVNIELKPKGQIARSAGASQVTKGSKYVLIIRLS 180
Db 119 GAEDAIKVGNALEKDPVGTIVVNIEMKPKGQIARSAGTSQVTKGSKYVLIIRLS 178
QY 181 GEVRMILSTRATIGQVGNLQHELVNKGKRSWKGRIPTRVRSVWNPNDHPHGGEGR 240
Db 179 GEVRMILATCATIGQVNEQHELVNKGKRSWKGRIPTRVRSVWNPNDHPHGGEGR 238
QY 241 APIGRSPMSPWGKPTLGKTRRKSSDKLIVGRKKK 279
Db 239 APIGRSPMSPWGKPTLGKTRKKNNSDKPIVRRKKK 277

RESULT 14

ABU32542
ID ABU32542 standard; protein; 277 AA.

XX AC ABU32542;

XX 19-JUN-2003 (first entry)

DE Protein encoded by *Prokaryotic essential gene #18069*.

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX *Listeria monocytogenes*.
OS WO200277183-A2.
XX 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
DR N-PSDB; ACA36412.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 60466; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 277 AA;

Query Match 82.6%; Score 1203; DB 6; Length 277;
Best Local Similarity 82.4%; Pred. No. 6.5e-112;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;

QY 1 MAIKKYPITNGRRNMTSLDPAETTKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60

Db 1 MAIKKYPITNGRRNMTSSDPAETTTTPKSLRPLPKKAGRNNOGKLTVRHHGGGHR 60

QY 61 QYRVDFKRNKOGINAKVDSIQYDPNRSANIALVYADGKRIYHCIAPKGLEVGQIVES 120

XX OS Staphylococcus epidermidis.
 XX PN US2004147734-A1.
 XX XX 29-JUL-2004.
 XX PF 01-DEC-2003; 2003US-00724972.
 XX PR 08-NOV-1997; 97US-0064964P.
 XX PR 13-AUG-1998; 98US-00134001.
 XX PR 29-NOV-1999; 99US-00450969.
 XX XX (DOUC/) DOUCETTE-STAMM L.
 XX PA (BUSH/) BUSH D.
 XX PI Doucette-Stamm L, Bush D;
 XX XX WPI; 2004-580138/56.
 XX DR N-PSDB; ADS03304.
 XX XX New isolated polypeptide and encoding nucleic acid derived from
 PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or
 PT treating an S. epidermidis bacterial infection.
 XX XX Claim 17; SEQ ID NO 6371; 741pp; English.
 XX CC The invention describes an isolated nucleic acid comprising a nucleotide
 CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:
 CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any
 CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as
 CC given in the specification. Also described are: a recombinant expression
 CC vector; a cell comprising a recombinant expression vector of (1);
 CC producing an S. epidermidis polypeptide; an isolated nucleic acid
 CC comprising a nucleotide sequence of at least 8 nucleotides in length; a
 CC vaccine composition for prevention or treatment of an S. epidermidis
 CC infection, comprising a nucleic acid cited above and a carrier; treating
 CC a subject for S. epidermidis infection; a recombinant or substantially
 CC pure preparation of an S. epidermidis polypeptide or its fragment; a
 CC vaccine composition for prevention or treatment of an S. epidermidis
 CC infection; detecting the presence of a Staphylococcus nucleic acid in a
 CC sample; a computer readable medium having recorded in it the nucleotide
 CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based
 CC system for identifying fragments of the Staphylococcus genome of
 CC commercial importance; a computer based system for identifying fragments
 CC of the Staphylococcus plasmids of commercial importance; identifying
 CC commercially important nucleic acid fragments of the Staphylococcus
 CC genome and/or plasmids; and identifying an expression modulating fragment
 CC of the Staphylococcus genome and/or plasmids. The methods and
 CC compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of an Staphylococcus epidermidis bacterial
 CC infection. This is the amino acid sequence of a S. epidermidis protein of
 CC the invention.
 XX XX Sequence 279 AA;
 XX SQ Query Match 94.4%; Score 1375; DB 8; Length 279;
 XX Best Local Similarity 93.5%; Pred. No. 3.6e-129;
 XX Matches 261; Conservative 12; Mismatches 4; Indels 2; Gaps 1;
 QY 1 MAIKKYKPTNGRRNMTSLDFAITKTPKSLKPLPKKAGRNNOGKLVRRHGGGSHKR 60
 Db 3 MAUKKYKPTNGRRNMTSLDFAITKTPKSLQPLPKRAGRNNOGKLVRRHGGGSHKR 62
 QY 61 QYRVDFKRNKDGINAKVDSIQDPNRSANIALVVYADGKRYTHCTAPKGLVGVQIVS 120
 Db 63 QYRVDFKRNKDGITAKVDSIQDPNRSANIALVVYADGKRYTHCTAPKGLVGVQIVS 120
 QY 121 GABADTKVGNALPLQNIIPVGTVVHNIETLKPCKGQIARSAGASQVLGKGGKVLRLRS 180
 Db 121 GABADTKVGNALPLQNIIPVGTVVHNIETLKPCKGQIARSAGASQVLGKGGKVLRLRS 180
 QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRSRWKGIPTVRGSMVNPNDPHGGGEGR 240

Db 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRSRWKGIPTVRGSMVNPNDPHGGGEGR 240
 QY 241 APIGRSPSPMPGKPTLGKKTTRGKSSDKLIVRGRKKK 279
 Db 241 APIGRSPSPMPGKPTLGKKTTRGKSSDKLIVRGRKKK 279
 RESULT 11
 ABJ19022
 ID ABJ19022 standard; protein; 277 AA.
 XX AC ABJ19022;
 XX XX 06-MAR-2003 (first entry)
 XX DE Pathogen specific antigen related staphylococcal protein SEQ ID No 271.
 XX KW Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
 KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
 KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
 KW autoimmune disease; HIV; hepatitis.
 XX OS Staphylococcus sp.
 XX PN WO200259148-A2.
 XX PD 01-AUG-2002.
 XX PF 21-JAN-2002; 2002WO-EP000546.
 XX PR 26-JAN-2001; 2001AT-00000130.
 XX PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
 XX PI Meinke A, Nagy E, Von Ahlsen U, Klade C, Henics T, Zauner W;
 PI Minh DB, Vytvytska O, Btz H, Dryla A, Weichhart T, Hafner M;
 PI Tempelmaier B;
 XX DR WPI; 2003-075410/07.
 XX PT Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 PT preventing e.g. staphylococcal infections, comprises providing antibody
 PT preparation.
 XX PS Example 7; Page 199; 252pp; English.
 XX CC The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the
 CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonisation against S. aureus or S. epidermidis. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against S. aureus or S. epidermidis. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention
 XX SQ Sequence 277 AA;
 XX Query Match 94.3%; Score 1373; DB 6; Length 277;
 XX Best Local Similarity 93.9%; Pred. No. 5.7e-129;
 XX Matches 262; Conservative 11; Mismatches 4; Indels 2; Gaps 1;

CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 277 AA;

Query Match 94.8%; Score 1380; DB 6; Length 277;
 Best Local Similarity 94.3%; Pred. No. 1.1e-129;
 Matches 263; Conservative 11; Mismatches 3; Indels 2; Gaps 1;
 QY 1 MAIKKYKPTITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
 DB 1 MALKKYKPTITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
 QY 61 QYRVDFKRNKOGINAKVDSIQYDPNRSANIALVTVADGKRIYHCIAPIKGLVGGQIVES 120
 DB 61 QYRVDFKRNKOGITAKVDSIQYDPNRSANIALVTVADGKRIYHCIAPIKGLVGGQIVES 118
 QY 121 GAADTKVGNALPLQNPVGTIVHNIETLPGKGQIARSAGASQVLGKGGKYLRLRS 180
 DB 119 GAADTKVGNALPLQNPVGTIVHNIETLPGKGQIARSAGASQVLGKGGKYLRLRS 178
 QY 181 GEVRMILSTCRATIGQVGNLQHELVNVGKAGSRWKGIPTVRGSMNPNNDHPHGGGEGR 240
 DB 179 GEVRMILSTCRATIGQVGNLQHELVNVGKAGSRWKGIPTVRGSMNPNNDHPHGGGEGR 238
 QY 241 APIGRSPSPMGKPTLGKTRGKSSDKLIVRGKKK 279
 DB 239 APIGRSPSPMGKPTLGKTRGKSSDKLIVRGKKK 277

RESULT 9
 ABP38415
 ID ABP38415 standard; protein; 279 AA.
 AC ABP38415;
 XX
 DT 24-JUL-2002 (first entry)
 DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3260.
 XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 KW Staphylococcus epidermidis; gene therapy.
 XX antibacterial; gene therapy.
 OS Staphylococcus epidermidis.

XX US6380370-B1.
 PN 30-APR-2002.
 XX 13-AUG-1998; 98US-00134001.
 XX 14-AUG-1997; 97US-0055779P.
 PR 08-NOV-1997; 97US-0064964P.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX Doucette-Stamm LA, Bush D;
 PI WPI; 2002-381255/41.
 DR N-PSDB; ABN90960.
 XX Novel isolated nucleic acid encoding a Staphylococcus epidermis
 PT polypeptide, useful for diagnosing and treating bacterial infections.
 XX Disclosure; SEQ ID NO 3260; 267pp; English.
 CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABP35124 to ABP37960. The *S. epidermidis* sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences can
 CC also be used in the diagnosis and treatment of bacterial infections,
 CC particularly *S. epidermidis* infections. The sequences can be used to
 CC screen for compounds able to interfere with the *S. epidermidis* life cycle
 CC or inhibit *S. epidermidis* infection. N.B. The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from the USPTO web site
 XX Sequence 279 AA;

Query Match 94.4%; Score 1375; DB 5; Length 279;
 Best Local Similarity 93.5%; Pred. No. 3.6e-129;
 Matches 261; Conservative 12; Mismatches 4; Indels 2; Gaps 1;
 QY 1 MAIKKYKPTITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
 DB 3 MALKKYKPTITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 62
 QY 61 QYRVDFKRNKOGINAKVDSIQYDPNRSANIALVTVADGKRIYHCIAPIKGLVGGQIVES 120
 DB 63 QYRVDFKRNKOGITAKVDSIQYDPNRSANIALVTVADGKRIYHCIAPIKGLVGGQIVES 120
 QY 121 GAADTKVGNALPLQNPVGTIVHNIETLPGKGQIARSAGASQVLGKGGKYLRLRS 180
 DB 121 GAADTKVGNALPLQNPVGTIVHNIETLPGKGQIARSAGASQVLGKGGKYLRLRS 180
 QY 181 GEVRMILSTCRATIGQVGNLQHELVNVGKAGSRWKGIPTVRGSMNPNNDHPHGGGEGR 240
 DB 181 GEVRMILSTCRATIGQVGNLQHELVNVGKAGSRWKGIPTVRGSMNPNNDHPHGGGEGR 240
 QY 241 APIGRSPSPMGKPTLGKTRGKSSDKLIVRGKKK 279
 DB 241 APIGRSPSPMGKPTLGKTRGKSSDKLIVRGKKK 279

RESULT 10
 ADS07076
 ID ADS07076 standard; protein; 279 AA.
 AC ADS07076;
 XX
 DT 04-NOV-2004 (first entry)
 DE Staphylococcus epidermis polypeptide seqid 6371.
 XX Staphylococcus epidermis; open reading frame; ORF; bacterial infection;
 KW Staphylococcus epidermis; gene therapy.
 XX antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;
 KW recombinant expression vector; infection; computer readable medium;
 KW computer based system.

CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 277 AA;

Query Match 97.0%; Score 1412; DB 6; Length 277;
Best Local Similarity 98.2%; Pred. No. 6.9e-133;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 1 MAIKKYKPIITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
DB 1 MAIKKYKPIITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
QY 61 QYRVIDPKRNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCTAPKGLVGVQIVES 120
DB 61 QYRVIDPKRNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCTAPKGLVGVQIVES 118
QY 121 GAADTKVGNALPLQNIPTVGTVVHNIELKPKGGQIARSAGASAOVLGKGGKYLIRLS 180
DB 119 GAADTKVGNALPLQNIPTVGTVVHNIELKPKGGQIARSAGASAOVLGKGGKYLIRLS 178
QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APIGRSPSPMSWGKPTLGKTRRGKSSDKLIVRGRKKK 279
DB 239 APIGRSPSPMSWGKPTLGKTRRGKSSDKLIVRGRKKK 277

RESULT 7

ABM72939
ID ABM72939 standard; protein; 277 AA.

XX AC ABM72939;

XX 20-NOV-2003 (first entry)

XX Staphylococcus aureus protein #2179.

XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX enzymatic assay; antibiotic target.

XX Staphylococcus aureus.

XX WO200294868-A2.

XX 28-NOV-2002.

XX 27-MAR-2002; 2002WO-IB002637.

XX 27-MAR-2001; 2001GB-00007661.

XX (CHIR-) CHIRON SPA.

XX Masignani V, Mora M, Scarselli M;

XX WPI; 2003-120786/11.

XX N-PSDB; ACF74499.

XX New Staphylococcus aureus protein, useful as a vaccine for treating or
XX preventing Staphylococcal infection, specifically an infection caused by
XX S. aureus, e.g. sepsis.

XX Claim 1; SEQ ID NO 4358; 49pp; English.

XX The invention relates to novel genes and encoded proteins from

XX Staphylococcus aureus. A composition comprising the S. aureus protein, a
XX nucleic acid encoding the protein, or an antibody to the protein, is
XX useful as a pharmaceutical, particularly as a vaccine for treating or
XX preventing infection due to Staphylococcus bacteria, specifically an

CC infection caused by S. aureus. The composition is particularly useful for
CC treating or preventing sepsis in a patient. The composition can also be
CC used for diagnostics. The protein is also used in an assay for enzymatic
CC studies and as a target for antibiotics. This sequence represents one of
CC the novel S. aureus proteins of the invention

XX SQ Sequence 277 AA;

Query Match 97.0%; Score 1412; DB 6; Length 277;
Best Local Similarity 98.2%; Pred. No. 6.9e-133;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 1 MAIKKYKPIITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
DB 1 MAIKKYKPIITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
QY 61 QYRVIDPKRNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCTAPKGLVGVQIVES 120
DB 61 QYRVIDPKRNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCTAPKGLVGVQIVES 118
QY 121 GAADTKVGNALPLQNIPTVGTVVHNIELKPKGGQIARSAGASAOVLGKGGKYLIRLS 180
DB 119 GAADTKVGNALPLQNIPTVGTVVHNIELKPKGGQIARSAGASAOVLGKGGKYLIRLS 178
QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVRMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APIGRSPSPMSWGKPTLGKTRRGKSSDKLIVRGRKKK 279
DB 239 APIGRSPSPMSWGKPTLGKTRRGKSSDKLIVRGRKKK 277

RESULT 8

ABU43554
ID ABU43554 standard; protein; 277 AA.

XX AC ABU43554;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #29081.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Staphylococcus haemolyticus.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 08-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA47424.

XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 71478; 1766pp; English.

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 222.
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
KW autoimmune disease; HIV; hepatitis.
XX
XX Staphylococcus sp.
OS
XX WO200259148-A2.
XX
XX
XX
XX 01-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-EP000546.
XX
XX 26-JAN-2001; 2001AT-00000130.
XX
XX (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
XX Meinke A, Nagy E, Von Ahsen U, Klade C, Henics T, Zauner W;
PI Minh DB, Vytvytska O, Btz H, Dryla A, Weichhart T, Hafner M;
PI Tempelmaier B;
XX
XX WPI; 2003-075410/07.
XX
XX Identifying, isolating and producing hyperimmune serum-reactive antigens
PT from a pathogen, for preparing vaccine or medicament for treating or
PT preventing e.g. staphylococcal infections, comprises providing antibody
PT preparation.
XX
XX Example 7; Page 186; 252pp; English.
XX
XX The invention relates to a novel method for identifying, isolating and
CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
CC allergen, a tissue or host prone to auto-immunity, where the antigens are
CC used in a vaccine, comprises providing antibody preparation from a plasma
CC pool of a type of animal, or individual sera with antibodies against the
CC specific pathogen, tumour, allergen, tissue or host prone to auto-
CC immunity. The hyperimmune serum-reactive antigens comprising any of the
CC 62 sequences of 53-2261 amino acids fully defined in the specification,
CC or their hyperimmune fragments are useful for the manufacture of a
CC pharmaceutical preparation, particularly a vaccine against staphylococcal
CC infections or colonisation against S. aureus or S. epidermidis. The
CC preparation of antibodies is useful for the manufacture of a medicament
CC for treating or preventing staphylococcal infections or colonisation
CC against S. aureus or S. epidermidis. The antibody preparations may also
CC be used for diagnostic and imaging purposes. Other conditions that can be
CC treated include cancer, autoimmune diseases or infections caused by viral
CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
CC sequence represents a staphylococcal protein relating to the method for
CC identifying and producing pathogen specific antigens of the invention
XX
XX Sequence 277 AA;
Query Match 97.0%; Score 1412; DB 6; Length 277;
Best Local Similarity 98.2%; Pred. No. 6.9e-133;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 1 MAIKKKYPTNGRNNTSLDPAITTKTTPKSLKLPKKGAGNNOKLTVRHGGGHR 60
DB 1 MAIKKKYPTNGRNNTSLDPAITTKTTPKSLKLPKKGAGNNOKLTVRHGGGHR 60
QY 61 QYRVDFPKRNGKGNKAKVDSIQVDNRSANIALVWYADGKRYTHCIAPKGLVGVQIVES 120
DB 61 QYRVDFPKRNGKGNKAKVDSIQVDNRSANIALVWYADGKR--YIAPKGLVGVQIVES 118
QY 121 GAEDATKVGNALPLQNPVGTVVHNIELPKGGQIARSAGASQVLGKGGKVLRLRS 180
DB 119 GAEDADKVGNALPLQNPVGTVVHNIELPKGGQIARSAGASQVLGKGGKVLRLRS 178
QY 181 GEVRMILSTCRATIGQVNLQHELNVNKGAGRSRWKGIPTVRSVWNPNDPHGGGGR 240
DB 179 GEVRMILSTCRATIGQVNLQHELNVNKGAGRSRWKGIPTVRSVWNPNDPHGGGGR 238

QY 241 APIGRSPSPMGKPTLGKTRRGKSSDKLIVRGKKK 279
DB 239 APIGRSPSPMGKPTLGKTRRGKSSDKLIVRGKKK 277
RESULT 6
ABU15836
ID ABU15836 standard; protein; 277 AA.
XX
XX ABU15836;
XX
XX 19-JUN-2003 (first entry)
XX
XX Protein encoded by Prokaryotic essential gene #1363.
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX Staphylococcus aureus.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX
XX 06-SEP-2001; 2001US-00948993.
XX
XX 25-OCT-2001; 2001US-0342923P.
XX
XX 08-FEB-2002; 2002US-00072851.
XX
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX
XX N-PSDB; ACA19706.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 43760; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of

PT antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 12767; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 277 AA;

Query Match 97.0%; Score 1412; DB 4; Length 277;
Best Local Similarity 98.2%; Pred. No. 6.9e-133;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 1 MAIKKYKPIITNGRRNMTSLDFAEITKTPKSLKPLPKKAGRNQKLTVRHHGGGHR 60
Db 1 MAIKKYKPIITNGRRNMTSLDFAEITKTPKSLKPLPKKAGRNQKLTVRHHGGGHR 60
QY 61 QYRVDFPKRNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVES 120
Db 61 QYRVDFPKRNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVES 118
QY 121 GAADATKVGNALPLQNI PVGT VVHNI ELKPKGQIARSAGASAOVLGKGGKYLIRLS 180
Db 119 GAADATKVGNALPLQNI PVGT VVHNI ELKPKGQIARSAGASAOVLGKGGKYLIRLS 178
QY 181 GEVRMILSTCRATIGQVGNLQHEL VNVGKAGSRWKGI RPTVRGSMVNPNDHPHGGEGR 240
Db 179 GEVRMILSTCRATIGQVGNLQHEL VNVGKAGSRWKGI RPTVRGSMVNPNDHPHGGEGR 238
QY 241 APIGRSPSPWGKPTLGKTRGKSSDKLIVRGRKK 279
Db 239 APIGRSPSPWGKPTLGKTRGKSSDKLIVRGRKK 277

RESULT 4

AAU34212
ID AAU34212 standard; protein; 277 AA.

XX AC AAU34212;

XX DT 14-FEB-2002 (first entry)

XX DE Staphylococcus aureus cellular proliferation protein #488.

XX KW Antisense; prokaryotic cellular proliferation protein; antibiotic;

XX KW antibacterial; drug design.

XX OS Staphylococcus aureus.

XX PN WO200170955-A2.

XX PD 27-SEP-2001.

XX FF 21-MAR-2001; 2001WO-US009180.

XX PR 21-MAR-2000; 2000US-0191078P.

XX PR 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlson KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
DR N-PSDB; AAS52071.

XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 5708; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes,
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 277 AA;

Query Match 97.0%; Score 1412; DB 4; Length 277;
Best Local Similarity 98.2%; Pred. No. 6.9e-133;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 1 MAIKKYKPIITNGRRNMTSLDFAEITKTPKSLKPLPKKAGRNQKLTVRHHGGGHR 60
Db 1 MAIKKYKPIITNGRRNMTSLDFAEITKTPKSLKPLPKKAGRNQKLTVRHHGGGHR 60
QY 61 QYRVDFPKRNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVES 120
Db 61 QYRVDFPKRNDGINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVES 118
QY 121 GAADATKVGNALPLQNI PVGT VVHNI ELKPKGQIARSAGASAOVLGKGGKYLIRLS 180
Db 119 GAADATKVGNALPLQNI PVGT VVHNI ELKPKGQIARSAGASAOVLGKGGKYLIRLS 178
QY 181 GEVRMILSTCRATIGQVGNLQHEL VNVGKAGSRWKGI RPTVRGSMVNPNDHPHGGEGR 240
Db 179 GEVRMILSTCRATIGQVGNLQHEL VNVGKAGSRWKGI RPTVRGSMVNPNDHPHGGEGR 238
QY 241 APIGRSPSPWGKPTLGKTRGKSSDKLIVRGRKK 279
Db 239 APIGRSPSPWGKPTLGKTRGKSSDKLIVRGRKK 277

RESULT 5

ABJ19004

ID ABJ19004 standard; protein; 277 AA.

XX AC ABJ19004;

XX DT 06-MAR-2003 (first entry)

XX

Db 1 MAIKYKPTITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
QY 61 QYRVDFKKNKOGINAKVDSIQYDPNRSANIALVVTADGEKRIYHCIAPKGLEVGQIVS 120
Db 61 QYRVDFKKNKOGINAKVDSIQYDPNRSANIALVVTADGEKRIYHCIAPKGLEVGQIVS 118
QY 121 GAEDATKVGNALPLQNI PVGTVVHNIELKPGKGQIARSAGASAQVLGKGGKTVLRLRS 180
Db 119 GAEDATKVGNALPLQNI PVGTVVHNIELKPGKGQIARSAGASAQVLGKGGKTVLRLRS 178
QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRSRWKGIPTVRGSMVNPNDHPHGGGEGR 240
Db 179 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRSRWKGIPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APIGRSPSPMGKPTLGKTRRGKSSDKLIIVRGKKK 279
Db 239 APIGRSPSPMGKPTLGKTRRGKSSDKLIIVRGKKK 277

RESULT 2

AAU36656
ID AAU36656 standard; protein; 277 AA.

XX AC AAU36656;
XX DT 14-FEB-2002 (first entry)
XX DE Staphylococcus aureus cellular proliferation protein #826.

XX KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX KW antibacterial; drug design.
XX OS Staphylococcus aureus.

XX PN WO200170955-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US009180.

XX PR 21-MAR-2000; 2000US-0191078P.

XX PR 23-MAY-2000; 2000US-0206848P.

XX PR 26-MAY-2000; 2000US-0207727P.

XX PR 23-OCT-2000; 2000US-0242578P.

XX PR 27-NOV-2000; 2000US-0253625P.

XX PR 22-DEC-2000; 2000US-0257931P.

XX PR 16-FEB-2001; 2001US-0269308P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX PI Yamamoto RT, Xu HH;

XX DR WPI; 2001-611495/70.

XX DR N-PSDB; AAS54515.

XX PT New polynucleotides for the identification and development of
XX PT antibiotics, comprise sequences of antisense nucleic acids.

XX PS Example 3; SEQ ID NO 12249; 51pp; English.

XX CC The invention relates to antisense inhibitors of genes essential to
XX CC prokaryotic cellular proliferation, their use in identifying the genes,
XX CC their use in the discovery of novel antibiotics, the essential genes
XX CC themselves and the encoded proteins. The prokaryotes used are Escherichia
XX CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX CC useful for the identification of potential new targets for antibiotic
XX CC development. The antisense nucleic acids can also be used to identify
XX CC proteins used in proliferation, to express these proteins, and to obtain
XX CC antibodies capable of binding to the expressed proteins. The proteins can
XX CC be used to screen compounds in rational drug discovery programmes. The

CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 277 AA;

Query Match 97.0%; Score 1412; DB 4; Length 277;

Best Local Similarity 98.2%; Pred. No. 6.9e-133; Mismatches 2; Gaps 1;
Matches 274; Conservative 1; Indels 2;

QY 1 MAIKYKPTITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
Db 1 MAIKYKPTITNGRRNMTSLDFAEITKTTPKSLKPLPKKAGRNNOGKLTVRHHGGGHR 60
QY 61 QYRVDFKKNKOGINAKVDSIQYDPNRSANIALVVTADGEKRIYHCIAPKGLEVGQIVS 120
Db 61 QYRVDFKKNKOGINAKVDSIQYDPNRSANIALVVTADGEKRIYHCIAPKGLEVGQIVS 118
QY 121 GAEDATKVGNALPLQNI PVGTVVHNIELKPGKGQIARSAGASAQVLGKGGKTVLRLRS 180
Db 119 GAEDATKVGNALPLQNI PVGTVVHNIELKPGKGQIARSAGASAQVLGKGGKTVLRLRS 178
QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRSRWKGIPTVRGSMVNPNDHPHGGGEGR 240
Db 179 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRSRWKGIPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APIGRSPSPMGKPTLGKTRRGKSSDKLIIVRGKKK 279
Db 239 APIGRSPSPMGKPTLGKTRRGKSSDKLIIVRGKKK 277

RESULT 3

AAU37174

ID AAU37174 standard; protein; 277 AA.

XX AC AAU37174;

XX DT 14-FEB-2002 (first entry)

XX DE Staphylococcus aureus cellular proliferation protein #1344.

XX KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX KW antibacterial; drug design.

XX OS Staphylococcus aureus.

XX PN WO200170955-A2.

XX PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US009180.

XX PR 21-MAR-2000; 2000US-0191078P.

XX PR 23-MAY-2000; 2000US-0206848P.

XX PR 26-MAY-2000; 2000US-0207727P.

XX PR 23-OCT-2000; 2000US-0242578P.

XX PR 27-NOV-2000; 2000US-0253625P.

XX PR 22-DEC-2000; 2000US-0257931P.

XX PR 16-FEB-2001; 2001US-0269308P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX PI Yamamoto RT, Xu HH;

XX DR WPI; 2001-611495/70.

XX DR N-PSDB; AAS55033.

XX PT New polynucleotides for the identification and development of

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 9, 2005, 15:48:59 ; Search time 161 Seconds
(without alignments)
670.225 Million cell updates/sec

Title: US-09-839-695B-13

Perfect score: 1456

Sequence: 1 MAIKKYKPIITNGRRNMTSLD.....KTRRGKSSDKLIVRGKKK 279

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1412	97.0	277	3	AAY70416 Staphyloc
2	1412	97.0	277	4	Aau36656 Staphyloc
3	1412	97.0	277	4	Aau37174 Staphyloc
4	1412	97.0	277	4	Aau34212 Staphyloc
5	1412	97.0	277	6	Abj19004 Pathogen
6	1412	97.0	277	6	Abu15836 Protein e
7	1412	97.0	277	6	Abm72939 Staphyloc
8	1380	94.8	277	6	Abu43554 Protein e
9	1375	94.4	279	5	Abp38415 Staphyloc
10	1375	94.4	279	8	Ads07076 Staphyloc
11	1373	94.3	277	6	Abj19022 Pathogen
12	1373	94.3	277	6	Abu42626 Protein e
13	1203	82.6	277	5	Abb49366 Listeria
14	1203	82.6	277	6	Abu32542 Protein e
15	1163	79.9	277	8	Ads44623 Bacterial
16	1154	79.3	276	8	Ads28071 Bacterial
17	1121	77.0	277	6	Abu46394 Protein e
18	1120	76.9	276	4	Aau34962 Enterococ
19	1120	76.9	276	6	Abu14500 Protein e
20	1117	76.7	277	5	Abp28608 Streptoco
21	1112	76.4	274	4	Aau33423 Enterococ
22	1108	76.1	277	4	Aau37607 Streptoco
23	1108	76.1	277	4	Aau37946 Streptoco
24	1108	76.1	277	6	Abu00552 S. pneumo
25	1108	76.1	277	6	Abp81521 Streptoco

ALIGNMENTS

RESULT 1

AAY70416

ID AAY70416 standard; protein; 277 AA.

XX AAY70416;

XX 21-JUN-2000 (first entry)

XX Staphylococcus aureus ribosomal protein RPL2.

XX S10-spc ribosomal operon; ribosomal protein; RPL2; screening; diagnosis;

KW antibacterial agent; treatment; prevention; bacterial infection.

XX Staphylococcus aureus.

XX WO200011184-A1.

XX 02-MAR-2000.

XX 23-AUG-1999; 99WO-US019298.

XX 25-AUG-1998; 98US-00139234.

XX (SCHE) SCHERING CORP.

XX Shimer GH, Hare RS, Shaw KJ, Black T;

XX WPI; 2000-256379/22.

XX N-PSDB; AAZ51566.

XX New Staphylococcus aureus polypeptides used for isolating antibacterial

PT agent for treating bacterial infections.

XX Claim 1; Page 28-29; 42pp; English.

XX The present sequence is a ribosomal protein RPL2 from S10-spc operon of

CC Staphylococcus aureus ATCC 55748. The protein is used as a target for

CC screening broad spectrum antibacterial agents which can be used to

CC prevent or treat diseases caused by bacteria. This sequence is also

CC useful in the diagnosis of bacterial infections

XX SQ Sequence 277 AA;

Query Match 97.0%; Score 1412; DB 3; Length 277;

Best Local Similarity 98.2%; Pred. No. 6.9e-133;

Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAIKKYKPIITNGRRNMTSLDFABITKTPEKSLKLPKPKAGRNQGLTVRRHGGGHR 60

Qy	238	EGR	P	I	G	R	P	S	P	M	S	P	W	G	K	P	T	L	G	K	T	R	R	G	K	S	S	D	K	L	I	V	R	G	K	278		
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
Db	239	E	G	K	O	P	I	G	R	K	A	P	L	T	P	W	G	K	K	A	L	G	V	K	T	R	D	N	K	S	T	K	L	I	R	R	K	279

RESULT 14

AE2332
50S ribosomal protein L2 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AB2332
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
N.; Tanaka, K.; Shimizu, T.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2332
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-287 <UNR>
A:Cross-references: KUNITPROT:Q8YP12; GB:BA000019; PIDN:BA875911.1; PID:gl7133347; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: rpl2
C:Superfamily: ribosomal protein L2/L8

Query Match 61.6%; Score 897; DB 2; Length 287;
Best Local Similarity 62.6%; Pred. No. 1.5e-63;
Matches 174; Conservative 35; Mismatches 67; Indels 2; Gaps 1;

Qy	1	MAIKYKPIITNGRNMVTS	DPAEITKTKTTPKSL	KLPKAGRNNOGKL	TVRHHGGGCHKR	60
Db	1	MGRSYRYPFPSTQVIT	SDISFAEITTEPKSL	TVYKRAKGRNNOGRI	TSRRGGGCHKR	60
Qy	61	QYRVIDFKRNKGINAK	VDGSIQVDPNRSANT	ALVYADGEKRI	VHCITAPKLEVGQIVES	120
Db	61	LYRIIDFKDRSIPATV	IAIEYDPNENARIAL	VSVEDEGKR	--YILHPNNLKVGTVIIA	118
Qy	121	GABADTKVGNALPLQ	NIPTVGTVVHNI	IBLKPCKGGQIARS	GASAOVJGKGKVVLI	180
Db	119	GPESPIEDGNALPL	ANIPLTGTSVHNEL	KAGKGGQIVRSAGA	TQVYVAKGENVYVTL	178
Qy	181	GEYRMILLSTRATIG	QVGNLQHELVN	YGKGRSWKGI	RPTVRGVSVMNPDH	240
Db	179	GEVRLTRRECVATIG	QVNTDARNLS	KAGKGRNWKGR	RRPKVRGVSVMNPDH	238
Qy	241	APIGRSPMSWGKPT	LTKTKTRGKSSD	KLIVRGKK	278	
Db	239	APIGRSGPVTWGKPT	LGAATRKPKKASS	KLIITRRRK	276	

RESULT 15

Ribosomal protein L2 U0234 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 07-Jul-2003
C:Accession: C82915
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mirror image of the complete sequence of Ureaplasma urealyticum: AAF30643.1; GSPDB:GN001
A;Reference number: A82870
A;Accession: C82915
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-279 <GLA>
A;Cross-references: GB:AE002123; GB:AF22894; NID:g6899229; PIDN:AAF30643.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C:Genetics:
A;Gene: rPL2; U0234
A;Genetic code: SGC3
C:Superfamily: ribosomal protein L2/L8


```
Db 1 MGIRVYKPTTNGRRNMTSLDFAEITTTPEKSLLVALKSKAGRNNGRIITVRHGGGHR 60
QY 61 QYRVIDFKRKGGINAKVDSIQYDPPNRANIALVYVADGSKRIYHCIAPKGLEVGQIVS 120
Db 61 FYRLVDFKRNKONVEAVVKTIYDPPNRANIALVHYTDGVKA--YIIAPKGLEVGQRIVS 118
QY 121 GAADTKVGNALPLQNIPIVGTVVVHNIELKPGKGQIARSAGASQAQVLGKGGKYLRLRS 180
Db 119 GPEADIKVGNALPLANIPVGTLLHNIELKPGRGELVRAAGASQAQVLGSEKGYLVRLOS 178
QY 181 GEVRMILSTCRATIGOVNLOHVLNVGKAGRSWKGIPTVRGSMVNPNDHPHGGEGR 240
Db 179 GEVRMILGTCTATVGVVGVNEQHLVNLGKAGRSWKGIPTVRGSMVNPNDHPHGGEGR 238
QY 241 APICRPSMPSPWGKPTLGKTRGKSSDKLIIVRGKKK 279
Db 239 APVGRKAPSTPWGKPALGLTRNKKAKSDKLIIVRRNEK 277

RESULT 8
G97895
50S ribosomal protein L2 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
R;Accession: G97895
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; H
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: G97895
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <L2>
A;Cross-references: UNIPROT:Q97SV2; UNIPROT:Q8CWV5; GB:AE007317; PIDN:AAK98995.1; PID:g1
C;Genetics:
A;Gene: rplB
A;Superfamily: ribosomal protein L2/L8

Query Match 76.1%; Score 1108; DB 2; Length 277;
Best Local Similarity 75.3%; Pred. No. 3e-80;
Matches 210; Conservative 26; Mismatches 41; Indels 2; Gaps 1;

QY 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLLVALKSKAGRNNGRIITVRHGGGHR 60
Db 1 MGIRVYKPTTNGRRNMTSLDFAEITTTPEKSLLVALKSKAGRNNGRIITVRHGGGHR 60
QY 61 QYRVIDFKRKGGINAKVDSIQYDPPNRANIALVYVADGSKRIYHCIAPKGLEVGQIVS 120
Db 61 FYRLVDFKRNKONVEAVVKTIYDPPNRANIALVHYTDGVKA--YIIAPKGLEVGQRIVS 118
QY 121 GAADTKVGNALPLQNIPIVGTVVVHNIELKPGKGQIARSAGASQAQVLGKGGKYLRLRS 180
Db 119 GPEADIKVGNALPLANIPVGTLLHNIELKPGRGELVRAAGASQAQVLGSEKGYLVRLOS 178
QY 181 GEVRMILSTCRATIGOVNLOHVLNVGKAGRSWKGIPTVRGSMVNPNDHPHGGEGR 240
Db 179 GEVRMILGTCTATVGVVGVNEQHLVNLGKAGRSWKGIPTVRGSMVNPNDHPHGGEGR 238
QY 241 APICRPSMPSPWGKPTLGKTRGKSSDKLIIVRGKKK 279
Db 239 APVGRKAPSTPWGKPALGLTRNKKAKSDKLIIVRRNEK 277

RESULT 9
H86886
50S ribosomal protein L2 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86886
```

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R;Bolotin, A.; Wincker, P.; Mauer, S.; Jaillon, O.; Malarre, K.; Weisenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86886
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <L2>
A;Cross-references: UNIPROT:Q9CDW5; GB:AE005176; PID:g12725150; PIDN:AAK06194.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: rplB
C;Superfamily: ribosomal protein L2/L8

Query Match 73.6%; Score 1072; DB 2; Length 276;
Best Local Similarity 74.8%; Pred. No. 2.1e-77;
Matches 205; Conservative 24; Mismatches 43; Indels 2; Gaps 1;

QY 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLLVALKSKAGRNNGRIITVRHGGGHR 60
Db 1 MGIRVYKPTTNGRRNMTSGDFAEITTTPEKSLLVSMKTAGRNNTGRITVRHGGGHR 60
QY 61 QYRVIDFKRKGGINAKVDSIQYDPPNRANIALVYVADGSKRIYHCIAPKGLEVGQIVS 120
Db 61 KIRVIDFKRTTNDVAKVAIIEYDPPNRANIALVIVSNGVKS--YIIAPKGLEVGQIVS 118
QY 121 GAADTKVGNALPLQNIPIVGTVVVHNIELKPGKGQIARSAGASQAQVLGKGGKYLRLRS 180
Db 119 GPEADIKVGNALPLANIPVGTLLHNIELKPGGQIVRSAGASQAQVLGSEKGYLVRLOS 178
QY 181 GEVRMILSTCRATIGOVNLOHVLNVGKAGRSWKGIPTVRGSMVNPNDHPHGGEGR 240
Db 179 GEVRMILSTCRATIGOVNLOHVLNVGKAGRSWKGIPTVRGSMVNPNDHPHGGEGR 238
QY 241 APICRPSMPSPWGKPTLGKTRGKSSDKLIIVR 274
Db 239 QVGRKSPMPWGKPALGLTRNKKAKSKLIIVR 272

RESULT 10
B54547
ribosomal protein l2 - mycoplasma-like organism MLO
C;Species: mycoplasma-like organisms, MLOs
C;Date: 06-Oct-1994 #sequence_revision 25-Apr-1997 #text_change 07-Jul-2003
C;Accession: B54547
R;Lim, P.O.; Searls, B.B.
FEBS Microbiol. Lett. 68, 71-73, 1991
A;Title: DNA sequence of the ribosomal protein genes rpl2 and rps19 from a plant-pathogen
A;Reference number: A54547; MUID:92120503; PMID:1769558
A;Accession: B54547
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <LIM>
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBI:77580, NCBI:77582)
C;Superfamily: ribosomal protein L2/L8

Query Match 66.7%; Score 971; DB 2; Length 276;
Best Local Similarity 68.0%; Pred. No. 2e-69;
Matches 189; Conservative 30; Mismatches 57; Indels 2; Gaps 1;

QY 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLLVALKSKAGRNNGRIITVRHGGGHR 60
Db 1 MAIKKYKPTTNGRRNMTSVAFSEITTTQTPKRLVSHKQAGRNNGRIITVRHGGGHR 60
QY 61 QYRVIDFKRKGGINAKVDSIQYDPPNRANIALVYVADGSKRIYHCIAPKGLEVGQIVS 120
Db 61 KYRLIDFKRNKONIVGKVAIIEYDPPNRANIALVHYLDGK--YIIAPKGLTVGMQIVS 118
QY 121 GAADTKVGNALPLQNIPIVGTVVVHNIELKPGKGQIARSAGASQAQVLGKGGKYLRLRS 180
Db 119 GKEADIKVGNALPLANIPVGTVVVHNIELKPGKGQIARSAGASQAQVLGKGGKYLRLRS 178
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C;Accession: AE1403
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative Genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1403
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <GLA>
A;Cross-references: UNIPROT:P60426; GB:NC_003210; PIDN:CAD00707.1; PID:g16412117; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: rplB
C;Superfamily: ribosomal protein L2/L8

Query Match 82.6%; Score 1203; DB 2; Length 277;
Best Local Similarity 82.4%; Pred. No. 9.1e-88;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;

QY 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLRLPKKAGRNNOGKLTVRHHGGGHR 60
DB 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLRLPKKAGRNNOGKLTVRHHGGGHR 60
QY 61 QYRVDFKRNKKGINAKVDSIOYDPNRSANIALVVTADGKRIYHCIAPKGLEVGQIVES 120
DB 61 QYRVDFKRNKKGIPORVATIEYDPNRSANIALVVTADGKRIYHCIAPKGLEVGQIYIS 118
QY 121 GAEADTKVGNALPLQNIPTVGVVHNIELKPGKGQIARSAGASAOVLGKGGKVLRLRS 180
DB 61 QYRVDFKRNKKGIPORVATIEYDPNRSANIALVVTADGKRIYHCIAPKGLEVGQIYIS 118
QY 181 GEVRMILSTCRATIGOVNQLQHELVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 240
DB 119 GAEADIKVGNALPLQNIPTVGVVHNIELKPGKGQIARSAGASAOVLGKGGKVLRLRS 178
QY 179 GEVRMILSTCRATIGOVNQLQHELVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVRMILSTCRATIGOVNQLQHELVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 240
QY 241 APIGRSPSPWGKPTLGKTRGKSSDKLIVRGKKK 279
DB 239 APIGRSPSPWGKPTLGKTRKNNNSDKFIVRRKKK 277

RESULT 3
AD1779
ribosomal protein L2 [imported] - *Listeria innocua* (strain Clp11262)
C;Species: *Listeria innocua*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1779
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative Genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1779
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <GLA>
A;Cross-references: UNIPROT:P60426; GB:AL592022; PIDN:CAC98004.1; PID:g16415314; GSPDB:
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: rplB
C;Superfamily: ribosomal protein L2/L8

Query Match 82.6%; Score 1203; DB 2; Length 277;
Best Local Similarity 82.4%; Pred. No. 9.1e-88;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;

QY 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLRLPKKAGRNNOGKLTVRHHGGGHR 60

DB 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLRLPKKAGRNNOGKLTVRHHGGGHR 60
QY 61 QYRVDFKRNKKGINAKVDSIOYDPNRSANIALVVTADGKRIYHCIAPKGLEVGQIVES 120
DB 61 QYRVDFKRNKKGIPORVATIEYDPNRSANIALVVTADGKRIYHCIAPKGLEVGQIYIS 118
QY 121 GAEADTKVGNALPLQNIPTVGVVHNIELKPGKGQIARSAGASAOVLGKGGKVLRLRS 180
DB 119 GAEADIKVGNALPLQNIPTVGVVHNIELKPGKGQIARSAGASAOVLGKGGKVLRLRS 178
QY 181 GEVRMILSTCRATIGOVNQLQHELVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVRMILSTCRATIGOVNQLQHELVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APIGRSPSPWGKPTLGKTRGKSSDKLIVRGKKK 279
DB 239 APIGRSPSPWGKPTLGKTRKNNNSDKFIVRRKKK 277

RESULT 4
F69694
ribosomal protein L2 (BL2) rplB - *Bacillus subtilis*
C;Species: *Bacillus subtilis*
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69694
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteck, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetcelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Segiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Torato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69694
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-277 <KUN>
A;Cross-references: UNIPROT:P42919; GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11895.1
A;Experimental source: strain 168
C;Genetics:
A;Gene: rplB
C;Superfamily: ribosomal protein L2/L8

Query Match 79.9%; Score 1163; DB 2; Length 277;
Best Local Similarity 79.9%; Pred. No. 1.3e-84;
Matches 223; Conservative 19; Mismatches 35; Indels 2; Gaps 1;

QY 1 MAIKKYKPTTNGRRNMTSLDFAEITTTPEKSLRLPKKAGRNNOGKLTVRHHGGGHR 60
DB 1 MAIKKYKPSNGRGNMTSLDFAEITTTPEKSLRLPLHKKGGNNNGKLTVRHGGGHR 60
QY 61 QYRVDFKRNKKGINAKVDSIOYDPNRSANIALVVTADGKRIYHCIAPKGLEVGQIVES 120
DB 61 QYRVDFKRNKKGIPORVATIEYDPNRSANIALVVTADGKRIYHCIAPKGLEVGQIYIS 118
QY 121 GAEADTKVGNALPLQNIPTVGVVHNIELKPGKGQIARSAGASAOVLGKGGKVLRLRS 180
DB 119 GAEADIKVGNALPLQNIPTVGVVHNIELKPGKGQIARSAGASAOVLGKGGKVLRLRS 178
QY 181 GEVRMILSTCRATIGOVNQLQHELVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVRMILSTCRATIGOVNQLQHELVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APIGRSPSPWGKPTLGKTRGKSSDKLIVRGKKK 279

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 9, 2005, 15:57:59 ; Search time 40 Seconds
(without alignments)
671.112 Million cell updates/sec

Title: US-09-839-695B-13
Perfect score: 1456
Sequence: 1 MAIKKYKPTNGRRNMTSLD.....KTRRGKSSDKLIVRGKKK 279

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1412	97.0	277	B90022	50S ribosomal prot
2	1203	82.6	277	AD1403	ribosomal protein
3	1203	82.6	277	AD1779	ribosomal protein
4	1163	79.9	277	F69694	ribosomal protein
5	1154	79.3	276	T44386	ribosomal protein
6	1125	77.3	275	R5BS2F	ribosomal protein
7	1108	76.1	277	G95024	ribosomal protein
8	1108	76.1	277	G97895	50S ribosomal prot
9	1072	73.6	276	H86886	50S ribosomal prot
10	971	66.7	276	B54547	ribosomal protein
11	969	66.6	277	B97285	ribosomal protein
12	958	65.8	281	R5YM2C	ribosomal protein
13	920.5	63.2	281	A99585	50S ribosomal prot
14	897	61.6	287	AE2332	50S ribosomal prot
15	895	61.5	279	C82915	ribosomal protein
16	885	60.8	275	B75534	ribosomal protein
17	880	60.4	280	C70642	probable ribosomal
18	876	60.2	274	C82059	ribosomal protein
19	871.5	59.9	276	A72250	ribosomal protein
20	862.5	59.2	274	R5EB2Y	ribosomal protein
21	862.5	59.2	274	AE0026	50S ribosomal prot
22	855	58.7	275	R5KT2	ribosomal protein
23	855	58.7	280	T45367	ribosomal protein
24	846	58.1	275	S78273	ribosomal protein
25	843	57.9	277	D82005	50S ribosomal prot
26	842	57.8	276	S77499	ribosomal protein
27	842	57.8	277	C81231	50S ribosomal prot
28	838	57.6	273	B83116	50S ribosomal prot
29	837.5	57.5	273	R5EC2	ribosomal protein

30	837.5	57.5	273	2	B85997	50S ribosomal subu
31	837.5	57.5	273	2	F91151	50S ribosomal subu
32	836.5	57.5	273	2	AD1006	50S ribosomal chai
33	834.5	57.3	273	2	H64092	ribosomal protein
34	823.5	56.6	273	2	F84990	50S ribosomal prot
35	819.5	56.3	276	2	D81268	50S ribosomal prot
36	816	56.0	277	2	S26081	ribosomal protein
37	813.5	55.9	277	2	H70159	ribosomal protein
38	812.5	55.8	275	2	C82177	50S ribosomal prot
39	810.5	55.7	294	2	S73232	ribosomal protein
40	806	55.4	275	2	T07361	ribosomal protein
41	806	55.4	285	2	A64217	ribosomal protein
42	786	54.0	277	1	R5LV2	ribosomal protein
43	782	53.7	273	2	B71355	probable ribosomal
44	781	53.6	287	2	S73989	ribosomal protein
45	774	53.2	277	2	AB3347	LSU ribosomal prot

ALIGNMENTS

RESULT 1

B90022
50S ribosomal protein L2 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B90022
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Uii, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B90022
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <KUR>
A;Cross-references: UNIPROT:P60432; GB:BA000018; PID:g13702047; PIDN:BA843339.1; GSPDB:G13702047
A;Experimental source: strain N315
C;Genetics:
A;Gene: rplB
C;Superfamily: ribosomal protein L2/L8

Query Match	97.0%	Score	1412;	DB	2;	Length	277;
Best Local Similarity	98.2%	Pred. No.	2.7e-104;				
Matches	274;	Conservative	1;	Mismatches	2;	Indels	2;
Gaps	1;						
Qy	1	MAIKKYKPTNGRRNMTSLDFAEITKTPPEKSLKPLPKKAGRNNOQKLTVRHHGGGHR	60				
Db	1	MAIKKYKPTNGRRNMTSLDFAEITKTPPEKSLKPLPKKAGRNNOQKLTVRHHGGGHR	60				
Qy	61	QYRVDFKRNKGINAKVDSIQYDNPNSANIALVWYADGKRIYHCIAPKGLEVGQIVES	120				
Db	61	QYRVDFKRNKGINAKVDSIQYDNPNSANIALVWYADGKRIYHCIAPKGLEVGQIVES	118				
Qy	121	GARADTKVGNALPLQNIPTVTVVHNIELKPKGQIARSAGASAOVLGKGGKYLIRLS	180				
Db	119	GARADTKVGNALPLQNIPTVTVVHNIELKPKGQIARSAGASAOVLGKGGKYLIRLS	178				
Qy	181	GEVRMILSTCRATIGQVGNLQHELNVNKGAGRWKGIPTVRGSMVNPNDHPHGGGEGR	240				
Db	179	GEVRMILSTCRATIGQVGNLQHELNVNKGAGRWKGIPTVRGSMVNPNDHPHGGGEGR	238				
Qy	241	APIGRSPMSPWGKPTLGKTRGKSSDKLIVRGKKK	279				
Db	239	APIGRSPMSPWGKPTLGKTRGKSSDKLIVRGKKK	277				

RESULT 2

AE1403
ribosomal protein L2 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

Search completed: June 9, 2005, 16:07:21
Job time : 176 secs

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DR EMBL; AP001507; BAB03856.1; -.
DR PIR; T44386; T44386.
DR HSP; P04257; 1RL2.
DR HAMAP; MF_01320; -. 1.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002171; Ribosomal_L2.
DR InterPro; IPR005880; Ribosomal_L2_b/o.
DR InterPro; IPR008991; Transl_SH3_like.
DR Pfam; PF00181; Ribosomal_L2; 1.
DR Pfam; PF03947; Ribosomal_L2_C; 1.
DR TIGRFAMs; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
SQ SEQUENCE 276 AA; 30224 MW; ABD31A20D6479696 CRC64;

Query Match 79.3%; Score 1154; DB 1; Length 276;
Best Local Similarity 78.4%; Pred. No. 2.9e-8;
Matches 216; Conservative 23; Mismatches 35; Indels 2; Gaps 1;

QY 1 MAIKKYKPTNGRRNMTSLDFAETTKTTPKSLKPLPKKAGRNQCKLTVRHGGGCHKR 60
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MAIKKYKPTNGRRNMTSLDFAETTKTTPKSLKPLPKKAGRNQCKLTVRHGGGCHKR 60

QY 61 QYRVDFPKRNDGINAKVDSIQYDPNRSANTALVYVADGKRIYHCIAPKGLEVGQIVES 120
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 QYRIIDFKRNDGIGPRVATIEYDPNRSANTALINYVDGKR--YILAPKGLKVGMTIES 118

QY 121 GAEDATKVGNALPLQNIPTVGTVVHNIELKPKGQGIARSAGASAOVLGKGGKYLIRLS 180
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
119 GAEDATKVGNALPLQNIPTVGTVVHNIELKPKGQGIARSAGASAOVLGKGGKYLIRLS 178

QY 181 GEVRMILSTCRATIGQVGNLOHLELVNKGAGRSWKGIPTVRGSMVNPNDHPHGGGEGR 240
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
179 GEVRLVLSACRATVGVGNESHELKIKGAGRSWLKGRPTVRGSMVNPNDHPHGGGEGR 238

QY 241 APIGRSPSPMGKPTLGKTRCKSSDKLIVGRKK 278
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
239 SPIGRKSPSPMGKPTLGKTRCKKASDKPIVRRKK 276

RESULT 15
RL2_BACAN
ID _RL2_BACAN STANDARD; PRT; 276 AA.
AC O61V57; O61471; O6KVH7;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name=rplB; OrderedLocusNames=BA0113, GBAA0113, BAS0113;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RX Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapfe E.K., Ostad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.B., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RC SEQUENCE=Ames / isolate 0581;
RP STRAIN=Ames;
```

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RA Ravel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RN Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=Stjerne;
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RA Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: One of the primary rRNA binding proteins. Required for
CC association of the 30S and 50S subunits to form the 70S ribosome,
CC for tRNA binding and peptide bond formation. It has been suggested
CC to have peptidyltransferase activity; this is somewhat
CC controversial. Makes several contacts with the 16S rRNA in the 70S
CC ribosome (By similarity).
CC -!- SUBUNIT: Part of the 70S ribosome (By similarity).
CC -!- SIMILARITY: Belongs to the ribosomal protein L2p family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE017024; AAP24167.1; -.
DR EMBL; AE017334; AAT29193.1; -.
DR EMBL; AE017225; AAT52450.1; -.
DR HSP; P04257; 1RL2.
DR TIGR; BA0113; -.
DR HAMAP; MF_01320; -. 1.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR002171; Ribosomal_L2.
DR InterPro; IPR005880; Ribosomal_L2_b/o.
DR InterPro; IPR008991; Transl_SH3_like.
DR Pfam; PF00181; Ribosomal_L2; 1.
DR Pfam; PF03947; Ribosomal_L2_C; 1.
DR TIGRFAMs; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
SQ SEQUENCE 276 AA; 30253 MW; FE3202D9F89FDE90 CRC64;

Query Match 78.2%; Score 1139; DB 1; Length 276;
Best Local Similarity 77.7%; Pred. No. 4.3e-81;
Matches 216; Conservative 22; Mismatches 38; Indels 2; Gaps 1;

QY 1 MAIKKYKPTNGRRNMTSLDFAETTKTTPKSLKPLPKKAGRNQCKLTVRHGGGCHKR 60
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MGIKKYNPTNGRRNMTTNDFAETTTDRPEKSLIAPLSKKAGRNQCKITVRHQGGCHKR 60

QY 61 QYRVDFPKRNDGINAKVDSIQYDPNRSANTALVYVADGKRIYHCIAPKGLEVGQIVES 120
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 QYRIIDFKRNDGIGPRVATIEYDPNRSANTALINYVDGKR--YILAPKKNLEVGMEIMS 118

QY 121 GAEDATKVGNALPLQNIPTVGTVVHNIELKPKGQGIARSAGASAOVLGKGGKYLIRLS 180
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
119 GAEDATKVGNALPLQNIPTVGTVVHNIELKPKGQGIARSAGASAOVLGKGGKYLIRLS 178

QY 181 GEVRMILSTCRATIGQVGNLOHLELVNKGAGRSWKGIPTVRGSMVNPNDHPHGGGEGR 240
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
179 GEVRLVLSACRATVGVGNESHELKIKGAGRSWLKGRPTVRGSMVNPNDHPHGGGEGR 238

QY 241 APIGRSPSPMGKPTLGKTRCKSSDKLIVGRKK 278
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
239 SPIGRKSPSPMGKPTLGKTRCKKASDKPIVRRKK 276
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Db 1 AIKKYPSNRRGMTSDFAEITTDKPEKSLIAPLHKGGRRNQKGLTVRHQGGGHKQ 60
QY 62 YRVIDFKRNDGINAKVDSIQYDNPNSANIALVYADGKRIYHCIAPKGLEVGQIVESG 121
Db 61 YRVIDFKRNDGINAKVDSIQYDNPNSANIALVYADGKRIYHCIAPKGLEVGQIVESG 118
QY 122 AADTKVGNALPONTIPVGTVNHIELKPKGGQIARSAGASAOVLGKGGKYLRLRS 181
Db 119 PEADIKVGNALPONTIPVGTVNHIELKPKGGQIARSAGASAOVLGKGGKYLRLRS 178
QY 182 EVRMILSTCRATIGQVGNLQHELHVLVNVGKAGSRWKGIRPTVRGSMVNPNDHPHGGGEGRA 241
Db 179 EVRMILSTCRATIGQVGNLQHELHVLVNVGKAGSRWKGIRPTVRGSMVNPNDHPHGGGEGRA 238
QY 242 PIGRSPSPMGKPTLGKTKRRGKSDKLIVRGRKK 279
Db 239 PIGRSPSPMGKPTLGKTKRRGKSDKLIVRGRKK 276
RESULT 13
RL2_OCEIH STANDARD; PRT; 276 AA.
AC OBETX9;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name=rpL2; OrderedLocusNames=OB0122;
OS Oceanobacillus ihayensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus ihayensis isolated from the Ihey Ridge and its unexpected adaptive capabilities to extreme environments.";
RT Nucleic Acids Res. 30:3927-3935(2002).
CC -!- FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for rRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome (By similarity).
CC -!- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the 30S subunit in the 70S ribosome (By similarity).
CC -!- SIMILARITY: Belongs to the ribosomal protein L2P family.
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CC EMBL; AP004593; BAC12078.1; -
DR HSSP; P04257; IRL2. -
DR HAWAP; MF_01320; -; 1.
DR InterPro; IPR008994; Nucleic acid OB.
DR InterPro; IPR002171; Ribosomal L2.
DR InterPro; IPR005880; Ribosomal L2 b/o.
DR InterPro; IPR008991; Transl SH3 like.
DR Pfam; PF00181; Ribosomal L2; 1.
DR Pfam; PF03947; Ribosomal L2_C; 1.
DR TIGRFAMs; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL L2; 1.
KW Complete proteome; Ribosomal protein; rRNA-binding; rRNA-binding.
SQ SEQUENCE 276 AA; 30386 MW; C9E5E6F0670F9CA0 CRC64;

Query Match

79.4%; Score 1156; DB 1; Length 276;

Best Local Similarity 78.8%; Pred. No. 2e-82;
Matches 219; Conservative 26; Mismatches 31; Indels 2; Gaps 1;
QY 1 MAIKKYKPTNGRRNMTSLDFAEITTDKPEKSLIAPLHKGGRRNQKGLTVRHQGGGHKQ 60
Db 1 MAIKKYKPTNGRRNMTSLDFAEITTDKPEKSLIAPLHKGGRRNQKGLTVRHQGGGHKQ 60
QY 61 QYRVIDFKRNDGINAKVDSIQYDNPNSANIALVYADGKRIYHCIAPKGLEVGQIVES 120
Db 61 QYRVIDFKRNDGINAKVDSIQYDNPNSANIALVYADGKRIYHCIAPKGLEVGQIVES 118
QY 121 GAEADTKVGNALPONTIPVGTVNHIELKPKGGQIARSAGASAOVLGKGGKYLRLRS 180
Db 119 GENADIKVGNALPONTIPVGTVNHIELKPKGGQIARSAGASAOVLGKGGKYLRLRS 178
QY 181 GEVRMILSTCRATIGQVGNLQHELHVLVNVGKAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 240
Db 179 GEVRMILSTCRATIGQVGNLQHELHVLVNVGKAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 238
QY 241 APGRSPSPMGKPTLGKTKRRGKSDKLIVRGRKK 278
Db 239 APGRSPSPMGKPTLGKTKRRGKSDKLIVRGRKK 276
RESULT 14
RL2_BACHD STANDARD; PRT; 276 AA.
AC Q929L1; Q9JPPY3;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name=rpL2; OrderedLocusNames=BH0137;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=99209008; PubMed=10192928;
RA Takami H., Takaki Y., Nakasone K., Hirama C., Inoue A., Horikoshi K.;
RT "Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125.";
RL Biosci. Biotechnol. Biochem. 63:452-455(1999).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hiramata C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -!- FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for rRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome (By similarity).
CC -!- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the 30S subunit in the 70S ribosome (By similarity).
CC -!- SIMILARITY: Belongs to the ribosomal protein L2P family.
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CC EMBL; AB017508; BAA75274.1; -

RA	Berka R.M.;
RT	"Complete genome sequence of the industrial bacterium Bacillus
RT	licheniformis and comparisons with closely related Bacillus species.";
RL	Genome Biol. 5:R77-R77(2004).
DR	EMBL; AE017333; AAU39110.1; -.
DR	EMBL; CP000002; AAU21765.1; -.
KW	Ribosomal protein.
SQ	SEQUENCE 277 AA; 30302 MW; A6B7DDE718936870 CRC64;
	Query Match 80.7%; Score 1175; DB 2; Length 277;
	Best Local Similarity 80.3%; Pred. No. 6.5e-84;
	Matches 224; Conservative 18; Mismatches 35; Indels 2; Gaps 1;
QY	1 MAIKKVKPIITNGRRNMTSLDFAEITTKTPKSLLPLPKKAGRNNQGKLTVRHGGGCHKR 60
Db	1 MAIKKVKPTSGRRGMTSSDFAEITTDQPEKSLAPLHKKGRRNQGLTVRHGGGCHKR 60
QY	61 QYRVIDFKRKNDGINAKVDSIQDPNSANIALVVYADGEKRIYHCITAPKGLEVGQIVES 120
Db	61 QYRIIIDFKRKDDIGPRVATVEYDPNSANIALINYVDGEKR--YILAPQLQGVGTIRMS 118
QY	121 GA8ADTKVGNALPIONTPVGTIVVHNIELKPGKGQIARSAAGASQAQLGKEGKYVLRLRS 180
Db	119 GP8ADIKVGNALPLINIPVGTIVVHNIELKPGKGQIVRSAGTSLQVLGKEGKYVLRLNS 178
QY	181 GEVRMILLSTCRATIGQVGNLQHLELVNYGKAGRSRWKGIPIPTVRGSVMNPNDHPHGCGEGR 240
Db	179 GEVRMILLSACRATIGQVNEQEHELINIGKAGRSRWKGVPIPTVRGSVMNPNDHPHGCGEGR 238
QY	241 APIGRSPSPMGWKPTTGKKTTRRGKKSSDKLIVRGKKK 279
Db	239 APIGRKSPMGWKPTLTGFTRKCKKNKSDKPIVRRRNK 277

RESULT 12	RL2_BACSU	STANDARD;	PRT; 276 AA.
ID	RL2_BACSU	STANDARD;	PRT; 276 AA.
AC	P42919;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	50S ribosomal protein L2 (BL2).		
DE	Name=sp1B; OrderedLocusNames=BSU01190;		
GN	Bacillus subtilis.		
OX	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OC	NCBI_TaxID=1423;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SG38;		
RC	MEDLINE=98037503; PubMed=9371452;		
RA	Li X., Lindahl L., Sha Y., Zengel J.M.;		
RA	"Analysis of the bacillus subtilis S10 ribosomal protein gene cluster		
RT	identifies two promoters that may be responsible for transcription of		
RT	the entire 15-kilobase S10-spc-alpha cluster.";		
RT	J. Bacteriol. 179:7046-7054(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=168;		
RC	MEDLINE=97124188; PubMed=8969501;		
RA	Yasumoto K., Liu H., Jeong S.M., Ohashi Y., Kakinuma S., Tanaka K.,		
RA	Kawamura F., Yoshikawa H., Takahashi H.;		
RT	"Sequence analysis of a 50 kb region between spo0H and rrnH on the		
RT	Bacillus subtilis chromosome.";		
RT	Microbiology 142:3039-3046(1996).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=168;		
RC	MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;		
RA	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,		
RA	Azevedo V., Bertsche M.G., Beeseters P., Solotini A., Borchert S.,		
RA	Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,		
RA	Chouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,		
RA	Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,		

[illegible]

CC -!- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
CC 30S subunit in the 70S ribosome (By similarity).
CC -!- SIMILARITY: Belongs to the ribosomal protein L2P family.
CC -----
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DR EMBL; AL591983; CAD00707.1; -.
DR PIR; AE1403; AE1403.
DR List; LMO02629; -.
DR HAMAP; MF_01320; -; 1.
DR InterPro; IPR002171; Ribosomal L2.
DR InterPro; IPR005880; Ribosomal L2_b/o.
DR TIGRFAMs; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein; rRNA-binding; rRNA-binding.
SQ SEQUENCE 277 AA; 30505 MW; DD05B498AF5A632 CRC64;

Query Match 82.6%; Score 1203; DB 1; Length 277;
Best Local Similarity 82.4%; Pred. No. 4.2e-86;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;

QY 1 MAIKYKPTNGRRNMTSLDFAITKTTPKSLKPLPKKAGNNOKLTVRHGGGHR 60
DB 1 MAIKYKPTNGRRNMTSLDFAITKTTPKSLKPLPKKAGNNOKLTVRHGGGHR 60
QY 61 QYRVDFKRNKDGINAKVDSIOVDNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
DB 61 QYRVDFKRNKDGIPGRVATIEYDNPNSANIALINLYADGEKR--YIIAAKLEVGQTIYS 118
QY 121 GABADTKVGNALPLQNPVGTVVHNIETLPGKGGQIARSAGASQVILGKGGKYLRLRS 180
DB 119 GABADTKVGNALPLQNPVGTVVHNIETLPGKGGQIARSAGASQVILGKGGKYLRLRS 178
QY 181 GEVRMTLSTCRATIGQVGNLQHELVNKGAGSRWGIPTVRGSMVNDHPHGGGEGR 240
DB 179 GEVRMTLATCRATIGQVGNLQHELVNKGAGSRWGIPTVRGSMVNDHPHGGGEGR 238
QY 241 APIGRSPSPWGKPTLGKTRGKSSDKLIIVRGKKK 279
DB 239 APIGRSPSPWGKPTLGKTRKNNNSDKFIVRRKKK 277

RESULT 10
QY1WE9 PRELIMINARY; PRT; 277 AA.
AC QY1WE9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein L2.
GN Name=rplB; OrderedLocusNames=LMOF2365_2602;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Unlich G.A.,
RA Bayles D.O., Luchansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
borne pathogen *Listeria monocytogenes* reveal new insights into the
core genome components of this species.";

RL Nucleic Acids Res. 32:2386-2395 (2004).
DR EMBL; AR017331; AAT05367.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0015934; C:large ribosomal subunit; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR008994; Nucleic acid OB.
DR InterPro; IPR002171; Ribosomal L2.
DR InterPro; IPR005880; Ribosomal L2_b/o.
DR InterPro; IPR008991; Transl_SH3_like.
DR Pfam; PF00181; Ribosomal L2; 1.
DR TIGRFAMs; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 277 AA; 30505 MW; DD05B498AF5A632 CRC64;

Query Match 82.6%; Score 1203; DB 2; Length 277;
Best Local Similarity 82.4%; Pred. No. 4.2e-86;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;

QY 1 MAIKYKPTNGRRNMTSLDFAITKTTPKSLKPLPKKAGNNOKLTVRHGGGHR 60
DB 1 MAIKYKPTNGRRNMTSLDFAITKTTPKSLKPLPKKAGNNOKLTVRHGGGHR 60
QY 61 QYRVDFKRNKDGINAKVDSIOVDNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
DB 61 QYRVDFKRNKDGIPGRVATIEYDNPNSANIALINLYADGEKR--YIIAAKLEVGQTIYS 118
QY 121 GABADTKVGNALPLQNPVGTVVHNIETLPGKGGQIARSAGASQVILGKGGKYLRLRS 180
DB 119 GABADTKVGNALPLQNPVGTVVHNIETLPGKGGQIARSAGASQVILGKGGKYLRLRS 178
QY 181 GEVRMTLSTCRATIGQVGNLQHELVNKGAGSRWGIPTVRGSMVNDHPHGGGEGR 240
DB 179 GEVRMTLATCRATIGQVGNLQHELVNKGAGSRWGIPTVRGSMVNDHPHGGGEGR 238
QY 241 APIGRSPSPWGKPTLGKTRGKSSDKLIIVRGKKK 279
DB 239 APIGRSPSPWGKPTLGKTRKNNNSDKFIVRRKKK 277

RESULT 11
QY6PA4 PRELIMINARY; PRT; 277 AA.
AC QY6PA4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE RplB (Ribosomal protein L2) (BL2).
GN Name=rplB; ORFNames=BL01049, BLI00136;
OS *Bacillus licheniformis* DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DSM 13;
RX PubMed=15383718;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of *Bacillus licheniformis* DSM13, an
Organism with Great Industrial Potential";
RL J. Mol. Microbiol. Biotechnol. 7:204-211 (2004).
RP [2]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

CC controversial. Makes severe
CC ribosome (By similarity).

CC controversial. Makes several contacts with the 16S rRNA in
CC ribosome (By similarity).


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KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
SQ SEQUENCE 277 AA; 30155 MW; F29296D3EE1E146E CRC64;

Query Match 97.0%; Score 1412; DB 1; Length 277;
Best Local Similarity 98.2%; Pred. No. 1.8e-102;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAIKKYPITNGRRNMTSLDFAEITKTPKSLKLPKPKAGRNNOGKLVRRHGGGHR 60
DB 1 MAIKKYPITNGRRNMTSLDFAEITKTPKSLKLPKPKAGRNNOGKLVRRHGGGHR 60

QY 61 QYRVDFPKRNOGINAKVDSIQYDPNRSANIALVYVADGKRIYHCITAPKGLVGVQIVES 120
DB 61 QYRVDFPKRNOGINAKVDSIQYDPNRSANIALVYVADGKRIYHCITAPKGLVGVQIVES 118

QY 121 GAADTKVGNALPLQNPVGTVVHNIELPKGGOIARSAGASQVLGKGGKYLRLRS 180
DB 119 GAADTKVGNALPLQNPVGTVVHNIELPKGGOIARSAGASQVLGKGGKYLRLRS 178

QY 181 GEVVMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVVMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 238

QY 241 APIGRSPSPMPGKPTLGKTRRGKSSDKLIVRGRKKK 279
DB 239 APIGRSPSPMPGKPTLGKTRRGKSSDKLIVRGRKKK 277

RESULT 4
RL2_STAAM STANDARD; PRT; 277 AA.
ID RL2_STAAM
AC P60433; Q99S24; Q9AJ03;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 23-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name=rlb; OrderedLocNames=MW2166;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RX Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -I- FUNCTION: One of the primary rRNA binding proteins. Required for
CC association of the 30S and 50S subunits to form the 70S ribosome.
CC for rRNA binding and peptide bond formation. It has been suggested
CC to have peptidyltransferase activity; this is somewhat
CC controversial. Makes several contacts with the 16S rRNA in the 70S
CC ribosome (By similarity).
CC -I- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
CC 30S subunit in the 70S ribosome (By similarity).
CC -I- SIMILARITY: Belongs to the ribosomal protein L2p family.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AP004829; BAB96031.1; -.
CC HSSP; P04257; IRL2.
CC HAMAP; MF_01320; -.
CC InterPro; IPR002171; Ribosomal_L2.
CC InterPro; IPR005880; Ribosomal_L2_b/o.
CC TIGRFAMs; TIGR01171; rplB_bact; 1.
CC PROSITE; PS00467; RIBOSOMAL_L2; 1.
DR
```

```
KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
SQ SEQUENCE 277 AA; 30155 MW; F29296D3EE1E146E CRC64;

Query Match 97.0%; Score 1412; DB 1; Length 277;
Best Local Similarity 98.2%; Pred. No. 1.8e-102;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAIKKYPITNGRRNMTSLDFAEITKTPKSLKLPKPKAGRNNOGKLVRRHGGGHR 60
DB 1 MAIKKYPITNGRRNMTSLDFAEITKTPKSLKLPKPKAGRNNOGKLVRRHGGGHR 60

QY 61 QYRVDFPKRNOGINAKVDSIQYDPNRSANIALVYVADGKRIYHCITAPKGLVGVQIVES 120
DB 61 QYRVDFPKRNOGINAKVDSIQYDPNRSANIALVYVADGKRIYHCITAPKGLVGVQIVES 118

QY 121 GAADTKVGNALPLQNPVGTVVHNIELPKGGOIARSAGASQVLGKGGKYLRLRS 180
DB 119 GAADTKVGNALPLQNPVGTVVHNIELPKGGOIARSAGASQVLGKGGKYLRLRS 178

QY 181 GEVVMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 240
DB 179 GEVVMILSTCRATIGQVGNLQHELNVNKGAGSRWKGIRPTVRGSMVNPNDHPHGGGEGR 238

QY 241 APIGRSPSPMPGKPTLGKTRRGKSSDKLIVRGRKKK 279
DB 239 APIGRSPSPMPGKPTLGKTRRGKSSDKLIVRGRKKK 277

RESULT 5
Q6G774 PRELIMINARY; PRT; 277 AA.
ID Q6G774
AC Q6G774;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE 50S ribosomal protein L2.
GN OrderedLocNames=SAS2138;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RX Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG43949.1; -.
DR GO; GO:0005822; C:intracellular; IEA.
DR GO; GO:0015934; C:large ribosomal subunit; IEA.
DR GO; GO:0003723; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR008994; Nucleic_acid__OB.
DR InterPro; IPR002171; Ribosomal_L2.
DR InterPro; IPR005880; Ribosomal_L2_b/o.
DR InterPro; IPR008991; Transl_S33__like.
DR Pfam; PF00181; Ribosomal_L2; 1.
DR Pfam; PF03947; Ribosomal_L2_C; 1.
DR TIGRFAMs; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 277 AA; 30155 MW; F29296D3EE1E146E CRC64;
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Best Local Similarity 98.2%; Pred. No. 1.8e-102;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAIKKYKPIINGRRNMTSLDPAETTKTTPKSKLLKPLPKKAGRNNOGKLTVRHHGGGCHKR 60
DB 1 MAIKKYKPIINGRRNMTSLDPAETTKTTPKSKLLKPLPKKAGRNNOGKLTVRHHGGGCHKR 60

QY 61 QYRVDFPKRKGKINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
DB 61 QYRVDFPKRKGKINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 118

QY 121 GAADTKVGNALPLONIPVGTVVHNIELKPKGGQIARSAGASAOVLGKGGKVLRLRS 180
DB 119 GAADTKVGNALPLONIPVGTVVHNIELKPKGGQIARSAGASAOVLGKGGKVLRLRS 178

QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRWKGIPTVRGSMVNPNDHPHGGEGR 240
DB 179 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRWKGIPTVRGSMVNPNDHPHGGEGR 238

QY 241 APIGRSPSPMGKPTLGKTKRGGKSSDKLIVRGKKK 279
DB 239 APIGRSPSPMGKPTLGKTKRGGKSSDKLIVRGKKK 277

RESULT 2

RL2 STAAU STANDARD; PRT; 277 AA.

ID RL2 STAAU STANDARD; PRT; 277 AA.
AC P60432; Q99S24; Q9AJ03;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name: rplB; Ordered locus names: SA2044;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP MEDLINE=21311952; PubMed=1418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshino K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
CC -I- FUNCTION: One of the primary rRNA binding proteins. Required for
CC association of the 30S and 50S subunits to form the 70S ribosome,
CC for rRNA binding and peptide bond formation. It has been suggested
CC to have peptidyltransferase activity; this is somewhat
CC controversial. Makes several contacts with the 16S rRNA in the 70S
CC ribosome (By similarity).
CC -I- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
CC 30S subunit in the 70S ribosome (By similarity).
CC -I- SIMILARITY: Belongs to the ribosomal protein L2P family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AP003136; BAB43339.1; -.
CC PIR; B90022; B90022.
CC HSP; P04257; IRL2.
CC HAMAP; MF 01320; -; 1.
CC InterPro; IPR002171; Ribosomal_L2.
CC DR PIR; B90022; B90022.
CC DR HAMAP; MF 01320; -; 1.
CC DR InterPro; IPR002171; Ribosomal_L2.
CC DR PIR; B90022; B90022.
CC DR HAMAP; MF 01320; -; 1.
CC DR InterPro; IPR002171; Ribosomal_L2 b/o.

DR TIGRFAMS; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein; rRNA-binding; rRNA-binding.
SQ SEQUENCE 277 AA; 30155 MW; F29296D3EE1E146E CRC64;

Query Match 97.0%; Score 1412; DB 1; Length 277;
Best Local Similarity 98.2%; Pred. No. 1.8e-102;
Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAIKKYKPIINGRRNMTSLDPAETTKTTPKSKLLKPLPKKAGRNNOGKLTVRHHGGGCHKR 60
DB 1 MAIKKYKPIINGRRNMTSLDPAETTKTTPKSKLLKPLPKKAGRNNOGKLTVRHHGGGCHKR 60

QY 61 QYRVDFPKRKGKINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 120
DB 61 QYRVDFPKRKGKINAKVDSIQYDPNRSANIALVYVADGKRIYHCIAPKGLEVGQIVS 118

QY 121 GAADTKVGNALPLONIPVGTVVHNIELKPKGGQIARSAGASAOVLGKGGKVLRLRS 180
DB 119 GAADTKVGNALPLONIPVGTVVHNIELKPKGGQIARSAGASAOVLGKGGKVLRLRS 178

QY 181 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRWKGIPTVRGSMVNPNDHPHGGEGR 240
DB 179 GEVRMILSTCRATIGQVGNLQHELNVNKGAGRWKGIPTVRGSMVNPNDHPHGGEGR 238

QY 241 APIGRSPSPMGKPTLGKTKRGGKSSDKLIVRGKKK 279
DB 239 APIGRSPSPMGKPTLGKTKRGGKSSDKLIVRGKKK 277

RESULT 3

RL2 STAAU STANDARD; PRT; 277 AA.

ID RL2 STAAU STANDARD; PRT; 277 AA.
AC P60430; Q99S24; Q9AJ03;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name: rplB;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA Balaban N.;
RA Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RL -I- FUNCTION: One of the primary rRNA binding proteins. Required for
RL association of the 30S and 50S subunits to form the 70S ribosome,
RL for rRNA binding and peptide bond formation. It has been suggested
RL to have peptidyltransferase activity; this is somewhat
RL controversial. Makes several contacts with the 16S rRNA in the 70S
RL ribosome (By similarity).
RL -I- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the
RL 30S subunit in the 70S ribosome (By similarity).
RL -I- SIMILARITY: Belongs to the ribosomal protein L2P family.
RL
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RL or send an email to license@isb-sib.ch).
RL
RL EMBL; AF205220; AAK37412.2; -.
RL HSP; P04257; IRL2.
RL HAMAP; MF 01320; -; 1.
RL InterPro; IPR002171; Ribosomal_L2.
RL PIR; B90022; B90022.
RL HAMAP; MF 01320; -; 1.
RL InterPro; IPR002171; Ribosomal_L2 b/o.

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OM protein - protein search, using sw model

Run on: June 9, 2005, 15:49:44 ; Search time 174 Seconds
(without alignments)
821.092 Million cell updates/sec

Title: US-09-839-695B-13
Perfect score: 1456
Sequence: 1 MAIKKYKPIINGRRNWTSLD.....KTRGKSSDKLIVGRKKK 279

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1412	97.0	277	1 RL2_STAAM	P60431 staphylococ
2	1412	97.0	277	1 RL2_STAAM	P60432 staphylococ
3	1412	97.0	277	1 RL2_STAAM	P60430 staphylococ
4	1412	97.0	277	1 RL2_STAAM	P60433 staphylococ
5	1412	97.0	277	2 Q6G774	Q6G774 staphylococ
6	1412	97.0	277	2 Q6G774	Q6G774 staphylococ
7	1373	94.3	277	1 RL2_STAAP	Q8crq3 staphylococ
8	1203	82.6	277	1 RL2_LISIN	P60435 listeria in
9	1203	82.6	277	1 RL2_LISMO	P60426 listeria mo
10	1203	82.6	277	2 Q71WE9	Q71WE9 listeria mo
11	1175	80.7	277	2 Q65PA4	Q65PA4 bacillus li
12	1158	79.5	276	1 RL2_BACSU	P42919 bacillus su
13	1156	79.4	276	1 RL2_OCEIH	Q8etx9 oceanobacil
14	1154	79.3	276	1 RL2_BACHD	Q82911 bacillus ha
15	1139	78.2	276	1 RL2_BACAN	Q81sv7 bacillus an
16	1139	78.2	276	2 Q63H87	Q63H87 bacillus ce
17	1139	78.2	276	2 Q73F93	Q73F93 bacillus ce
18	1139	78.2	276	2 Q6HP05	Q6HP05 bacillus th
19	1137	78.1	276	1 RL2_BACCR	Q81j39 bacillus th
20	1125	77.3	275	1 RL2_BACST	P04257 bacillus st
21	1121	77.0	277	1 RL2_STRF8	Q879r0 streptococc
22	1121	77.0	277	1 RL2_STRF8	P60435 streptococc
23	1121	77.0	277	1 RL2_STRFY	P60434 streptococc
24	1120	76.9	276	1 RL2_ENTFA	Q839g1 enterococcu
25	1108	76.1	277	1 RL2_STRPN	Q97sv2 streptococc
26	1108	76.1	277	1 RL2_STR6	Q8cw5 streptococc
27	1104	75.8	277	1 RL2_STR3A	Q8e7t5 streptococc
28	1104	75.8	277	1 RL2_STRAS	Q8e2c8 streptococc
29	1088	74.7	279	1 RL2_LACPL	Q88xy3 lactobacill
30	1072	73.6	276	1 RL2_LACLA	Q9cdw5 lactococcu
31	1022	70.2	275	1 RL2_THETN	Q8r7v7 thermoanaer

32	1014	69.6	278	2 Q74L86	Q74L86 lactobacill
33	1010	69.4	275	2 Q8GB24	Q8ge24 heliobacill
34	994	68.3	276	1 RL2_ONYPE	P60402 onion yello
35	979	67.2	276	1 RL2_ASTYP	Q50264 aster yello
36	975.5	67.0	281	1 RL2_MYCHO	Q8gm57 mycoplasma
37	969	66.6	277	1 RL2_CLOAB	Q97e11 clostridium
38	964.5	66.2	281	2 Q6F121	Q6f121 mesoplasma
39	962.5	66.1	277	2 Q67JU6	Q67ju6 symbiobacte
40	959	65.9	277	1 RL2_CLOPE	Q8xh6 clostridium
41	957	65.7	282	2 Q6MSW8	Q6msw8 mycoplasma
42	956	65.7	278	1 RL2_SPIKU	P60404 spiroplasma
43	954.5	65.6	283	2 Q6KI52	Q6ki52 mycoplasma
44	924	63.5	276	1 RL2_CLOTE	Q890pl clostridium
45	920.5	63.2	281	1 RL2_MYCPU	Q98py4 mycoplasma

ALIGNMENTS

RESULT 1

RL2_STAAM STANDARD; PRT; 277 AA.
AC P60431; Q99S24; Q9AJ03;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L2.
GN Name=rlpB; OrderedLocustNames=SAV2247;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus";
RL Lancel 357:1225-1240(2001).
CC -!- FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for rRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome (By similarity).
CC -!- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the 30S subunit in the 70S ribosome (By similarity).
CC -!- SIMILARITY: Belongs to the ribosomal protein L2P family.

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CC EMBL; AP003364; BAB58409.1; -;
DR HSSP; P04257; IRL2.
DR HAMAP; MF 01320; -; 1.
DR InterPro; IPR002171; Ribosomal_L2.
DR InterPro; IPR005880; Ribosomal_L2_b/o.
DR TIGRFAms; TIGR01171; rplB_bact; 1.
DR PROSITE; PS00467; RIBOSOMAL_L2; 1.
KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
SQ SEQUENCE 277 AA; 30155 MW; F29296D3EE1E146E CRC64;

Query Match 97.0%; Score 1412; DB 1; Length 277;